providing the DNA fragment as an insert within a plasmid host [that allows amplification in *E. coli*].

3. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, wherein introducing at least one fragment of DNA further comprises:

providing the DNA fragment as a linear fragment.

4. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, wherein introducing at least one fragment of DNA further comprises:

inserting the DNA fragment into a plasmid vector.

6. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 1, wherein the known length of the DNA fragment [complies with a protocol and where the protocol] is [selected from the group of protocols consisting of] (1) a length of DNA which provides PCR product(s) of known lengths when used with appropriate oligonucletide primers [as known in the art], in a PCR reaction in conjunction with short tandem repeats analysis, (2) a length of DNA which provides PCR product(s) of known lengths when used with appropriate oligonucletide primers [as known in the art], in a PCR reaction in conjunction with variable numbers of tandem repeats analysis, (3) a length of DNA which can be detected with defined nucleic acid probes when used in restriction fragment length polymorphisms, [and] or (4) a length of DNA which generates a unique known DNA sequence when used with the appropriate oligonucleotide sequencing primer(s) [as known in the art] with mitochondrial sequencing.

8. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 wherein the DNA fragment has binding sites for two different primers.

9. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 6 wherein a first DNA fragment is inserted into a first plasmid vector and a second DNA fragment is inserted into a second plasmid vector.

10. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 9, wherein the first DNA fragment and the second DNA fragment each have binding sites for two different primers.

11. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 6, wherein the DNA fragment has at least one attribute selected from the [list of attributes] group consisting of (1) the DNA fragment has a stability comparable to the [shelf life] stability of the biological [specimens] sample, (2) the DNA fragment in conjunction with primers used in the addition thereof does not interfere with the subsequent analysis of the known biological sample, (3) the DNA fragment in conjunction with primers used in the addition thereof does not produce any polymerase chain reaction products, restriction fragments, bands detected by hybridization analysis, or DNA sequence other than expected for the added DNA fragment, (4) the DNA fragment is compatible with, and stable through, standard DNA preparation procedures [as known in the art], (5) the concentration of the DNA fragment is of a predetermined amount such that it will be present in molar ratios similar to those of the analysis targets in the known biological samples after preparation of the sample for analysis and (6) the DNA fragment, or products generated from the DNA fragment, is compatible with at least one of DNA hybridization analysis, agarose gel electrophoresis, polyacrylamide gel electrophoresis, capillary electrophoresis, or matrix assisted laser desorption ionization time-of-flight mass spectrometry.

12. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 11, wherein the DNA fragment is added to a collection vessel.

13. (Amended) [The] A process for marking biological samples used in subsequent nucleic acid analysis comprising:

introducing at least one fragment of deoxyribonucleic acid (DNA) of known length and sequence into a collection vessel;

collecting at least one known biological sample;

adding the known biological sample[s] to the collection vessel to obtain a modified biological sample;

extracting the DNA from the modified sample to obtain extracted DNA;

providing primers complementary to the extracted DNA to obtain a resulting sample;

analyzing the resulting sample using [an assay] a technique selected from the [list of assay techniques] group consisting of polymerase chain reaction-based analysis of short tandem repeats; polymerase chain reaction-based analysis of variable numbers of tandem repeats; DNA hybridization analysis of restriction fragment length polymorphisms; and the sequencing of mitochondrial DNA.

18. (Amended) The process for marking biological samples used in subsequent nucleic acid analysis of claim 13, wherein the primers are supplied as components of assay kits.

REMARKS

Claims 1-18 were originally presented. Claims 1-18 were rejected. Claims 1-4, 6, 8-13, and 18 have been amended. Thus, original claims 5, 7, and 15-17, and amended claims 1-4, 6, 8-13, and 18 are currently pending.

I. Formal Matters

A. 35 U.S.C. §112